

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2004, 11:07:32 ; Search time 21 Seconds

(without alignments)  
82,450 Million cell updates/sec

Title: US-09-847-586-77

Sequence: 1 AKSPVKEAKSPKAKSP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	30	2	S02571
2	89	100.0	332	2	B43427
3	89	100.0	606	2	A43427
4	89	100.0	1020	1	QFNUH
5	76	85.4	854	2	S02003
6	76	85.4	1072	1	A37221
7	76	85.4	1087	1	QFMSH
8	61	68.5	532	1	QFPM
9	59.5	66.9	916	2	A27864
10	56	62.9	20	2	I53671
11	52	58.4	942	2	UC7316
12	51.5	57.9	6442	2	T29757
13	51	57.3	288	2	T06257
14	49	55.1	659	2	B87719
15	49	55.1	849	2	S00030
16	49	55.1	1200	2	A46194
17	48.5	54.5	219	1	HSNUB
18	48	53.9	206	1	HSTRIR
19	48	53.9	218	1	HSCCH
20	48	53.9	218	2	A23055
21	48	53.9	218	2	S01262
22	48	53.9	220	2	A28456
23	48	53.9	221	2	S33219
24	48	53.9	223	2	S49492
25	48	53.9	226	1	S51660
26	48	53.9	845	2	A45665
27	48	53.9	858	2	S15762
28	48	53.9	1208	2	T05077
29	47.5	53.4	209	1	HSX11A

30	47.5	53.4	221	2	S49482	histone H1 - mouse
31	47.5	53.4	229	2	I51227	histone H1A - Afri
32	47.5	53.4	248	1	HSURIP	histone H1, gonada
33	47	52.8	219	2	C28456	histone H1.11R - C
34	47	52.8	224	2	D28456	histone H1.03 - ch
35	47	52.8	225	2	B28456	histone H1.11L - C
36	47	52.8	476	2	S57963	methy1 CpG binding
37	47	52.8	492	2	A41907	histone H1B - Afri
38	46.5	52.2	219	1	HSX11B	histone H1B - Afri
39	46.5	52.2	220	2	I51447	histone H1B - Afri
40	46.5	52.2	221	1	B40335	histone H1-3 [vali
41	46.5	52.2	236	2	S22322	histone H1 - wheac
42	46	51.7	212	2	A28470	histone H1 - mouse
43	46	51.7	284	2	T06241	histone H1 (clone
44	46	51.7	1356	2	T16754	hypothetical prote
45	45.5	51.1	196	1	HSX15A	histone H5A - Afri

#### ALIGNMENTS

##### RESULT 1

S02571 neurofilament triplet protein H - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 10-Dec-1999

C:Accession: S02571

R:Gelsler, N.; Vandekerckhove, J.; Weber, K.

FEBS Lett. 221, 403-407, 1987

A:Title: Location and sequence characterization of the major phosphorylation sites of the

A:Reference number: S02570; PMID:8730485; PMID:3114005

A:Accession: S02571

A:Molecule type: protein

A:Residues: 1-30 <GEI>

A:Experimental source: spinal cord

A:Note: 5-Glu, 19-Glu, and 21-Glu were also found

C:Superfamily: neurofilament triplet H protein

C:Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein

F3.17/Binding site: phosphate (Ser) (covalent) #stratus experimental

Query Match 100.0%; Score 89; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKSPVKEAKSPKAKSP 18

Db 1 AKSPVKEAKSPKAKSP 18

##### RESULT 2

B43427 neurofilament protein H form H2 (repetitive region) - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 10-Jul-1998

C:Accession: B43427

R:Soppet, D.R.; Beasley, L.J.; Willard, M.B.

J. Biol. Chem. 267, 17354-17361, 1992

A:Title: Evidence for unequal crossing over in the evolution of the neurofilament polypep

A:Reference number: A43427; PMID:2381055; PMID:1512270

A:Accession: B43427

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-332 <SOP>

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIP:112012)

C:Superfamily: neurofilament triplet H protein

Query Match 100.0%; Score 89; DB 2; Length 332;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKSPVKEAKSPKAKSP 18

|||||

Db 84 AKSPVKEAKSPKAKSP 101

### RESULT 3

A43427

neurofilament triplet H1 protein - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 10-Dec-1999

C/Accession: A43427

R/Sopet, D.R.; Beasley, L.L.; Willard, M.B.

J. Biol. Chem. 267, 17354-17361, 1992

A/Title: Evidence for unequal crossing over in the evolution of the neurofilament polypeptide

A/Reference number: A43427; PMID:22381055; PMID:1512270

A/Accession: A43427

A/Molecule type: DNA

A/Residues: 1-606 <SOP>

A/Cross-references: GB:M94315; NID:G164990; PIDN:AAA57152.1; PID:G601930

A/Experimental source: brain

A/Note: sequence extracted from NCBI backbone (NCBI:112010, NCBI:112011)

C/Superfamily: neurofilament triplet H protein

C/Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein

Query Match

Best Local Similarity 100.0%; Score 89; DB 2; Length 606;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSPVKEAKSPKAKSP 18

92 AKSPVKEAKSPKAKSP 109

### RESULT 4

QFH0H

neurofilament triplet H protein - human

N/Alternate names: neurofilament protein, 112K

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-2000

C/Accession: S00979

R/Lees, J.F.; Sheldman, P.S.; Skuntz, S.F.; Carden, M.J.; Lazzarini, R.A.

EMBO J. 7, 1947-1955, 1988

A/Title: The structure and organization of the human heavy neurofilament subunit (NF-H)

A/Reference number: S00979; PMID:88328981; PMID:3138108

A/Accession: S00979

A/Molecule type: DNA

A/Residues: 1-1020 <HEE>

A/Cross-references: EMBL:X15306; NID:G35028; PIDN:CAA33366.1; PID:G1841430

A/Note: It is uncertain whether Met-1 or Met-2 is the initiator

C/Genetics:

A/Gene: GDB:NEFH

A/Cross-references: GDB:120225; OMIM:162230

A/Map position: 22q12.1-22q13.1

A/Intons: 295/1; 361/3; 403/2

C/Superfamily: neurofilament triplet H protein

C/Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein

F:1-100/Domain: amino-terminal <NID>

F:101-410/Domain: rod #status predicted <ROD>

F:411-1020/Domain: carboxyl-terminal <CTD>

F:502-826/Region: 14-residue repeats

F:503-511, 518-526, 532-540, 546-552, 560-566, 574-580, 586-594, 600-606, 614-620, 628-634, 640-644

(covalent) #status predicted

F:732,768/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 89; DB 1; Length 1020;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSPVKEAKSPKAKSP 18

694 AKSPVKEAKSPKAKSP 711

### RESULT 5

S02003

neurofilament triplet H protein - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 13-Aug-1999

C/Accession: S02003

R/Breen, K.C.; Robinson, P.A.; Wion, D.; Anderson, B.H.

FEBS Lett. 241, 213-218, 1988

A/Title: Partial sequence of the rat heavy neurofilament polypeptide (NF-H). Identification

A/Reference number: S02003; PMID:89065087; PMID:3143606

A/Accession: S02003

A/Molecule type: mRNA

A/Residues: 1-854 <BR>

A/Cross-references: EMBL:X13804; NID:G57828; PIDN:CAA32038.1; PID:G57829

C/Superfamily: neurofilament triplet H protein

C/Keywords: coiled coil

Query Match

Best Local Similarity 85.4%; Score 76; DB 2; Length 854;

Matches 18; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 AKSPVKE-----EAKSPKAKSP 18

525 AKSPVKEAKSLAEKSPKAKSP 548

### RESULT 6

A37221

neurofilament triplet H protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Dec-1999

C/Accession: A37221; A25649; A30796; A32757; B25649

R/Chin, S.S.M.; Liem, R.K.H.

J. Neurosci. 10, 3714-3726, 1990

A/Title: Transfected rat high-molecular-weight neurofilament (NF-H) coassembles with vim

A/Reference number: A37221; PMID:91038277; PMID:2230955

A/Accession: A37221

A/Status: Preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1072 <CHI>

A/Cross-references: GB:AF031879; NID:G2642597; PIDN:AB87068.1; PID:G2642598

R/Robinson, P.A.; Wion, D.; Anderson, B.H.

FEBS Lett. 209, 203-205, 1986

A/Title: Isolation of a cDNA for the rat heavy neurofilament polypeptide (NF-H).

A/Reference number: A25649; PMID:87080760; PMID:2878828

A/Accession: A25649

A/Molecule type: mRNA

A/Residues: 230-318; 472-542 <ROB>

A/Cross-references: GB:M37227

R/Dautigny, A.; Pham-Dinh, D.; Rousset, C.; Felix, J.M.; Nussbaum, J.L.; Jolles, P.

Biochem. Biophys. Res. Commun. 154, 1099-1106, 1988

A/Title: The large neurofilament subunit (NF-H) of the rat: cDNA cloning and in situ det

A/Reference number: A30796; PMID:88309090; PMID:2457365

A/Accession: A30796

A/Molecule type: mRNA

A/Residues: 266-421, 'T', 423-427, 'T', 429-542, 'V', 556-566, 'E', 568-613, 'A', 615-725, 'S', 727-

A/Cross-references: GB:M21964; NID:G205665; PIDN:AAA41695.1; PID:G205666

R/Liebetrug, I.; Spiller, N.; Spiller, S.; Anderson, U.; Goldgaber, D.; Smulowitz, M.; C

Proc. Natl. Acad. Sci. U.S.A. 86, 2463-2467, 1989

A/Title: Cloning of a cDNA encoding the rat high molecular weight neurofilament peptide

22.

A/Reference number: A32757; PMID:89184647; PMID:2928342

A/Accession: A32757

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 559-566, 'E', 568-967, 'V', 969-997, 'GST', 1001-1022, 'E', 1024-1072 <LIE>

A/Cross-references: GB:U04517; NID:G205679; PIDN:AAA41692.1; PID:G205680

C/Superfamily: neurofilament triplet H protein

C/Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein

Query Match

Best Local Similarity 85.4%; Score 76; DB 1; Length 1072;

Matches 18; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 AKSPVKE-----EAKSPKAKSP 18

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OM protein - protein search, using SW model

Run on: May 25, 2004, 11:14:43 ; Search time 42 Seconds

(without alignments)  
119.538 Million cell updates/sec

Title: US-09-847-586-77

Perfect score: 89

Sequence: 1 AKSPVKEAKSPKAKSP 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/BCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	18	10	US-09-847-586-13
2	89	100.0	18	10	US-09-847-586-71
3	89	100.0	18	10	US-09-847-586-72
4	89	100.0	18	10	US-09-847-586-73
5	89	100.0	18	10	US-09-847-586-74
6	89	100.0	18	10	US-09-847-586-75
7	89	100.0	18	10	US-09-847-586-76
8	89	100.0	18	10	US-09-847-586-77
9	89	100.0	19	10	US-09-847-586-78
10	89	100.0	617	9	US-09-847-586-78
11	89	100.0	617	14	US-10-029-386-32114
12	79	88.8	18	10	US-09-847-586-12
13	79	88.8	18	10	US-09-847-586-63
14	79	88.8	18	10	US-09-847-586-64
15	79	88.8	18	10	US-09-847-586-65

16	79	88.8	18	10	US-09-847-586-66	Sequence 66, Appl
17	79	88.8	18	10	US-09-847-586-67	Sequence 67, Appl
18	79	88.8	18	10	US-09-847-586-68	Sequence 68, Appl
19	79	88.8	18	10	US-09-847-586-69	Sequence 69, Appl
20	79	88.8	18	10	US-09-847-586-70	Sequence 70, Appl
21	65	73.0	16	10	US-09-847-586-47	Sequence 47, Appl
22	65	73.0	16	10	US-09-847-586-48	Sequence 48, Appl
23	65	73.0	16	10	US-09-847-586-49	Sequence 49, Appl
24	65	73.0	16	10	US-09-847-586-50	Sequence 50, Appl
25	65	73.0	16	10	US-09-847-586-51	Sequence 51, Appl
26	65	73.0	16	10	US-09-847-586-52	Sequence 52, Appl
27	65	73.0	16	10	US-09-847-586-53	Sequence 53, Appl
28	65	73.0	16	10	US-09-847-586-54	Sequence 54, Appl
29	64	71.9	16	10	US-09-847-586-22	Sequence 22, Appl
30	64	71.9	16	10	US-09-847-586-23	Sequence 23, Appl
31	64	71.9	16	10	US-09-847-586-24	Sequence 24, Appl
32	64	71.9	16	10	US-09-847-586-25	Sequence 25, Appl
33	64	71.9	16	10	US-09-847-586-26	Sequence 26, Appl
34	64	71.9	16	10	US-09-847-586-27	Sequence 27, Appl
35	64	71.9	16	10	US-09-847-586-28	Sequence 28, Appl
36	64	71.9	16	10	US-09-847-586-29	Sequence 29, Appl
37	64	71.9	16	10	US-09-847-586-30	Sequence 30, Appl
38	64	71.9	16	10	US-09-847-586-31	Sequence 31, Appl
39	64	71.9	16	10	US-09-847-586-32	Sequence 32, Appl
40	64	71.9	16	10	US-09-847-586-33	Sequence 33, Appl
41	59	66.3	18	10	US-09-847-586-34	Sequence 34, Appl
42	59	66.3	18	10	US-09-847-586-35	Sequence 35, Appl
43	59	66.3	18	10	US-09-847-586-36	Sequence 36, Appl
44	59	66.3	18	10	US-09-847-586-37	Sequence 37, Appl
45	59	66.3	18	10	US-09-847-586-38	Sequence 38, Appl

## ALIGNMENTS

RESULT 1

US-09-847-586-13

Sequence 13, Application US/09847586

Publication No. US20030148404A1

GENERAL INFORMATION:

APPLICANT: Michaelson

TITLE OF INVENTION: Peptides and substances, methods and devices using same

FILE REFERENCE: 01/21573

CURRENT APPLICATION NUMBER: US/09/847,586

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: PCT IL00/00509

PRIOR FILING DATE: 2000-08-27

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-847-586-13

Query Match 100.0%; Score 89; DB 10; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.5e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSPVKEAKSPKAKSP 18

Db 1 AKSPVKEAKSPKAKSP 18

RESULT 2

US-09-847-586-71

Sequence 71, Application US/09847586

Publication No. US20030148404A1

GENERAL INFORMATION:

Qy		1 AKSPVKEEAKSPEKAKSP	18
Db	1 AKSPVKEEAKSPEKAKSP	18	

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OM protein - protein search, using SW model

Run on: May 25, 2004, 11:12:23 ; Search time 23 Seconds

(without alignments)  
40.403 Million cell updates/sec

Title: US-09-847-586-77

Perfect score: 89

Sequence: 1 AKSPVKBAKSPBAKSP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.5	66.9	160	2	US-08-726-306A-68
2	51.5	57.9	35	3	US-08-995-172-18
3	48.5	54.5	26	3	US-08-894-339-6
4	48.5	54.5	26	3	US-09-306-044-6
5	48.5	54.5	218	3	US-09-041-889-4
6	48.5	54.5	218	3	US-08-837-058-4
7	48.5	54.5	218	3	US-09-417-264-4
8	48.5	53.9	61	1	US-08-346-889-17
9	48.5	53.9	61	2	US-08-293-284A-17
10	48.5	53.9	61	4	US-08-898-300-17
11	48.5	53.9	116	3	US-09-041-889-38
12	48.5	53.9	116	4	US-09-417-264-38
13	48.5	53.9	158	4	US-09-041-889-40
14	48.5	53.9	158	4	US-09-417-264-40
15	48.5	53.9	222	3	US-09-041-889-3
16	48.5	53.9	222	3	US-08-837-058-3
17	48.5	53.9	222	4	US-09-417-264-3
18	48.5	53.9	226	4	US-09-041-889-32
19	48.5	53.9	226	4	US-09-417-264-32
20	48.5	53.9	712	2	US-08-468-576B-17
21	48.5	53.9	712	2	US-08-468-576B-17
22	48.5	53.9	712	3	US-08-468-576B-17
23	47.5	53.4	60	1	US-08-346-849-16
24	47.5	53.4	60	2	US-08-293-284A-16
25	47.5	53.4	60	4	US-08-898-300-16
26	46.5	52.2	30	3	US-08-995-172-11
27	46.5	52.2	33	3	US-08-839-624-23

28	46.5	52.2	33	4	US-09-150-812-23	Sequence 23, Appl
29	46.5	52.2	60	2	US-08-769-211-2	Sequence 2, Appl
30	46.5	52.2	61	3	US-08-895-172-6	Sequence 6, Appl
31	46.5	52.2	61	3	US-08-995-172-7	Sequence 7, Appl
32	46.5	52.2	113	3	US-09-041-889-14	Sequence 14, Appl
33	46.5	52.2	113	3	US-08-837-058-14	Sequence 14, Appl
34	46.5	52.2	113	4	US-09-417-264-14	Sequence 14, Appl
35	46.5	52.2	147	3	US-09-041-889-13	Sequence 13, Appl
36	46.5	52.2	147	3	US-08-837-058-13	Sequence 13, Appl
37	46.5	52.2	147	4	US-09-417-264-13	Sequence 13, Appl
38	46.5	52.2	220	3	US-09-041-889-2	Sequence 2, Appl
39	46.5	52.2	220	3	US-08-837-058-2	Sequence 2, Appl
40	46.5	52.2	220	4	US-09-417-264-2	Sequence 2, Appl
41	45.5	51.1	26	2	US-08-894-339-9	Sequence 9, Appl
42	45.5	51.1	26	3	US-09-306-044-9	Sequence 9, Appl
43	45	50.6	194	4	US-09-125-619-28	Sequence 28, Appl
44	45	50.6	212	4	US-09-125-619-48	Sequence 48, Appl
45	45	50.6	214	4	US-09-125-619-35	Sequence 35, Appl

## ALIGNMENTS

RESULT 1  
US-08-726-306A-68  
Sequence 68, Application US/08726306A  
Patent No. 5958684  
GENERAL INFORMATION:  
APPLICANT: van Leeuwen, Frederik Willem  
APPLICANT: Burbach, Johannes Peter Henri  
APPLICANT: Grosfeld, Franklin G.  
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1 Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,306A  
FILING DATE: 02-Oct-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 95/20080.4  
FILING DATE: 02-Oct-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,832  
FILING DATE: 01-Jan-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 160 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-726-306A-68  
Query Match 66.9%; Score 59.5; DB 2; Length 160;  
Best Local Similarity 58.3%; Pred. No. 0.17;  
Matches 14; Conservative 2; Mismatches 1; Indels 7; Gaps 1;

QY 2 KSPVKEAKSP-----EKASP 18  
|||:|  
Db 131 KSPVKEAKSPVSKSPVKEAKSP 154

RESULT 2  
US-08-995-172-18  
Sequence 18, Application US/08995172B  
Patent No. 6218112  
GENERAL INFORMATION:  
APPLICANT: Thatcher, David R  
APPLICANT: Milks, Paula E  
TITLE OF INVENTION: Optimization of Gene Delivery and Gene Delivery Systems  
FILE REFERENCE: CACO0026  
CURRENT APPLICATION NUMBER: US/08/995,172B  
CURRENT FILING DATE: 1997-12-22  
EARLIER APPLICATION NUMBER: 60/033,908  
EARLIER FILING DATE: 1996-12-23  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentm Ver. 2.1  
SEQ ID NO 18  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (35)  
OTHER INFORMATION: Xaa is Cys with Acm sidechain  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide  
US-08-995-172-18

Query Match 57.9%; Score 51.5; DB 3; Length 35;  
Best Local Similarity 44.8%; Pred. No. 0.49;  
Matches 13; Conservative 2; Mismatches 3; Indels 11; Gaps 1;

QY 1 AKSPVKEA-----KSPVKEAKSP 18  
|||:|  
Db 3 AKSPAKAKAKVAKPKAKPKPKAKKP 31

RESULT 3  
US-08-894-339-6  
Sequence 6, Application US/08894339  
Patent No. 5945400  
GENERAL INFORMATION:  
APPLICANT: SHERMAN, Daniel  
APPLICANT: BYK, Gerardo  
TITLE OF INVENTION: SCHWARTZ, Bertrand  
TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION,  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, Mailstop 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentm Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,339  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/01865  
FILING DATE: 17-FEB-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR96/00248  
FILING DATE: 15-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky Esq., Martin F.  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: ST95012-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3816  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 6  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-894-339-6

Query Match 54.5%; Score 48.5; DB 2; Length 26;  
Best Local Similarity 63.2%; Pred. No. 0.97;  
Matches 12; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 AKSPVKEAKSPVKA-KSP 18  
|||:|  
Db 3 AKSPKAKAKAKPKAKPKSP 21

RESULT 4  
US-09-306-044-6  
Sequence 6, Application US/09306044  
Patent No. 6200956  
GENERAL INFORMATION:  
APPLICANT: SHERMAN, Daniel  
APPLICANT: BYK, Gerardo  
TITLE OF INVENTION: SCHWARTZ, Bertrand  
TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION,  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, Mailstop 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentm Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/306,044  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/894,339  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR96/00248  
FILING DATE: 15-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky Esq., Martin F.  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: ST95012-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3816  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 6  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

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OM protein - protein search, using sw model

Run on: May 25, 2004, 10:40:52 ; Search time 55 Seconds  
(without alignments)  
92.470 Million cell updates/sec

Title: US-09-847-586-77

Perfect score: 89  
Sequence: 1 AKSPYKAKSPKAKSP 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%

Listing first 45 summaries

Database: A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*\n2: Geneseqp1990s:\*\n3: Geneseqp2000s:\*\n4: Geneseqp2001s:\*\n5: Geneseqp2002s:\*\n6: Geneseqp2003s:\*\n7: Geneseqp2003bs:\*\n8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	18	5	ABB09392 Synthetic
2	89	100.0	18	5	ABB09396 Synthetic
3	89	100.0	18	5	ABB09393 Synthetic
4	89	100.0	18	5	ABB09395 Synthetic
5	89	100.0	18	5	ABB09390 Synthetic
6	89	100.0	18	5	ABB09394 Synthetic
7	89	100.0	18	5	ABB09389 Synthetic
8	89	100.0	18	5	ABB09391 Synthetic
9	89	100.0	19	5	ABB09397 Synthetic
10	89	100.0	617	4	AA16458 Peptide #
11	89	100.0	617	4	ABB35445 Peptide #
12	89	100.0	617	4	ABB20884 Peptide #
13	89	100.0	617	4	AA565629 Human bra
14	89	100.0	617	4	AA565305 Human liv
15	89	100.0	617	4	AA565305 Human liv
16	89	100.0	1020	7	AA663408 Human pro
17	89	100.0	1020	7	AA663408 Human pro
18	89	100.0	1026	4	AA178825 Human tes
19	89	100.0	1033	4	AA178825 Human tes
20	79	88.8	18	5	ABB09382 Synthetic
21	79	88.8	18	5	ABB09383 Synthetic
22	79	88.8	18	5	ABB09387 Synthetic
23	79	88.8	18	5	ABB09385 Synthetic
24	79	88.8	18	5	ABB09384 Synthetic
25	79	88.8	18	5	ABB09381 Synthetic

26	79	88.8	18	5	ABB09386 Synthetic
27	79	88.8	18	5	ABB09380 Synthetic
28	79	88.8	19	5	ABB09388 Synthetic
29	76	85.4	354	4	ABU52998 Human tes
30	76	85.4	373	4	ABU52996 Human tes
31	76	85.4	530	4	ABU52995 Human tes
32	76	85.4	622	4	ABU52993 Human tes
33	76	85.4	628	4	ABU52994 Human tes
34	76	85.4	831	7	AD63406 Rat Prote
35	76	85.4	831	7	AD63406 Rat Prote
36	76	85.4	831	7	AD63406 Rat Prote
37	76	85.4	1072	5	AD63406 Rat Prote
38	76	85.4	1072	5	AD63406 Rat Prote
39	75	84.3	420	4	ABU52997 Human tes
40	75	84.3	16	5	ABB09369 Synthetic
41	65	73.0	16	5	ABB09362 Synthetic
42	65	73.0	16	5	ABB09363 Synthetic
43	65	73.0	16	5	ABB09366 Synthetic
44	65	73.0	16	5	ABB09367 Synthetic
45	65	73.0	16	5	ABB09365 Synthetic
			5		ABB09364 Synthetic

#### ALIGNMENTS

RESULT 1	
ID	ABB09392 standard; peptide; 18 AA.
XX	XX
AC	ABB09392;
DT	01-JUL-2002 (first entry)
XX	XX
DS	Synthetic neurofilament peptide 8R.
XX	XX
KW	NP-H; neurodegenerative disorder; immunogenic epitope; nootropic;
KW	neuroprotective; antiparkinsonian; cerebroprotective; vasotropic;
KW	Alzheimer's disease; multi-infarct dementia; Pick's disease;
KW	frontotemporal dementia; dementia pugilistica; vascular dementia;
KW	Parkinson's disease; Gerstmann-Strausler-Scheinker disease;
KW	multiple sclerosis; Amyotrophic lateral sclerosis;
KW	transient ischemic attack; stroke; NP-M; Tau; B-amyloid protein.
XX	XX
OS	Synthetic.
XX	XX
FT	Key
FT	Modified site 17
FT	/note= "phosphorylated residue"
XX	XX
PN	MO200115655-A2.
XX	XX
PD	08-MAR-2001.
XX	XX
PF	27-AUG-2000; 2000MO-IL000509.
XX	XX
PR	31-AUG-1999; 99US-00386347.
XX	XX
PR	27-JUL-2000; 2000US-0221150P.
XX	XX
PA	(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PI	Michaelson DM;
XX	XX
DR	WPI; 2002-179260/23.
XX	XX
PT	Identifying existence, non-existence, type or state of neurodegenerative
PT	disorder, by reacting with serum a peptide derived from protein
PT	associated with the disorder, to which antibody is produced at onset of
PT	disorder.
XX	XX
PS	Claim 54; Page 43; 117pp; English.
XX	XX
CC	The invention relates to identifying existence, non-existence, type or
CC	state of neurodegenerative disorder (ND) in individual, involving

immunoreacting with serum derived from an individual, a peptide representing an epitope derived from endogenous protein to which an antibody (Ab) is produced in vivo at onset or during progression of ND, where Ab immunobinds with the peptide and detecting presence, absence or degree of immunobinding. Activity of the immunogenic peptides of the invention may be described as: nootropic, neuroprotective, antiparkinsonian, cerebroprotective and vasotropic. The peptides of the state of ND in an individual, where ND is associated with progressive loss of cognitive functions or motoric functions, or progressive loss of control of motoric functions. Such diseases include: Alzheimer's disease, Multi-infarct dementia (MID), Pick's disease, frontotemporal dementias, dementia pugilistica, vascular dementia, Parkinson's disease, Gerstmann-Strausler-Scheinker disease with tangles, multiple sclerosis, Amyotrophic lateral sclerosis (ALS), transient ischaemic attack (TIA) and stroke. In a preferred embodiment of the present invention, the endogenous protein is selected from the group consisting of NF-H, NF-M, Tau and B-amyloid protein. The current sequence represents a synthetic neurofilament peptide derived from the carboxy terminal of NF-H, for use as an immunogenic epitope. From each of the peptides represented in records ABB09325, ABB09334, ABB09343, ABB09353, ABB09362, ABB09371, ABB09380 AND ABB09390, can be generated 8 peptides in different states of phosphorylation, giving a total of 64 peptides (see ABB09325-ABB09397) covering all possible states of phosphorylation of the NF-H carboxy terminal domain

Sequence 18 AA:

Query Match 100.0%; Score 89; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSPVKEAKSPERAKSP 18  
1 AKSPVKEAKSPERAKSP 18

RESULT 2  
ABB09396  
ID ABB09396 standard; peptide; 18 AA.

AC ABB09396;  
DT 01-JUL-2002 (first entry)

XX Synthetic neurofilament peptide 8LMR.

XX NF-H; neurodegenerative disorder; immunogenic epitope; nootropic;  
XX neuroprotective; antiparkinsonian; cerebroprotective; vasotropic;  
XX Alzheimer's disease; multi-infarct dementia; Pick's disease;  
XX frontotemporal dementia; dementia pugilistica; vascular dementia;  
XX Parkinson's disease; Gerstmann-Strausler-Scheinker disease;  
XX multiple sclerosis; Amyotrophic lateral sclerosis;  
XX transient ischaemic attack; stroke; NF-M; Tau; B-amyloid protein.

XX Synthetic.

XX Key Location/Qualifiers  
XX Modified-site 3 /note= "phosphorylated residue"  
XX Modified-site 11 /note= "phosphorylated residue"  
XX Modified-site 17 /note= "phosphorylated residue"  
XX PN WO200115655-A2.  
XX 08-MAR-2001.  
XX 27-AUG-2000; 2000WO-11000509.  
XX 31-AUG-1999; 99US-00386347.  
XX 27-JUL-2000; 2000US-0221150P.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.  
XX Michaelson DM;  
XX WPI; 2002-179260/23.

XX Identifying existence, non-existence, type or state of neurodegenerative  
XX disorder, by reacting with serum a peptide derived from protein  
XX associated with the disorder, to which antibody is produced at onset of  
XX disorder.

XX Example 1; Page 43; 117bp; English.

XX The invention relates to identifying existence, non-existence, type or  
XX state of neurodegenerative disorder (ND) in individual, involving  
XX immunoreacting with serum derived from an individual, a peptide  
XX representing an epitope derived from endogenous protein to which an  
XX antibody (Ab) is produced in vivo at onset or during progression of ND,  
XX where Ab immunobinds with the peptide and detecting presence, absence or  
XX degree of immunobinding. Activity of the immunogenic peptides of the  
XX invention may be described as: nootropic, neuroprotective,  
XX antiparkinsonian, cerebroprotective and vasotropic. The peptides of the  
XX invention are useful for identifying existence, non-existence, type or  
XX state of ND in an individual, where ND is associated with progressive  
XX loss of cognitive functions or motoric functions, or progressive loss of  
XX control of motoric functions. Such diseases include: Alzheimer's disease,  
XX Multi-infarct dementia (MID), Pick's disease, frontotemporal dementias,  
XX dementia pugilistica, vascular dementia, Parkinson's disease, Gerstmann-  
XX Strausler-Scheinker disease with tangles, multiple sclerosis,  
XX Amyotrophic lateral sclerosis (ALS), transient ischaemic attack (TIA) and  
XX stroke. In a preferred embodiment of the present invention, the  
XX endogenous protein is selected from the group consisting of NF-H, NF-M,  
XX Tau and B-amyloid protein. The current sequence represents a synthetic  
XX neurofilament peptide derived from the carboxy terminal of NF-H, for use  
XX as an immunogenic epitope. From each of the peptides represented in  
XX records ABB09325, ABB09334, ABB09343, ABB09353, ABB09362, ABB09371,  
XX ABB09380 AND ABB09390, can be generated 8 peptides in different states of  
XX phosphorylation, giving a total of 64 peptides (see ABB09325-ABB09397)  
XX covering all possible states of phosphorylation of the NF-H carboxy  
XX terminal domain

Sequence 18 AA:

Query Match 100.0%; Score 89; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSPVKEAKSPERAKSP 18  
1 AKSPVKEAKSPERAKSP 18

RESULT 3  
ABB09393  
ID ABB09393 standard; peptide; 18 AA.

AC ABB09393;

DT 01-JUL-2002 (first entry)

XX Synthetic neurofilament peptide 8LM.

XX NF-H; neurodegenerative disorder; immunogenic epitope; nootropic;  
XX neuroprotective; antiparkinsonian; cerebroprotective; vasotropic;  
XX Alzheimer's disease; multi-infarct dementia; Pick's disease;  
XX frontotemporal dementia; dementia pugilistica; vascular dementia;  
XX Parkinson's disease; Gerstmann-Strausler-Scheinker disease;  
XX multiple sclerosis; Amyotrophic lateral sclerosis;  
XX transient ischaemic attack; stroke; NF-M; Tau; B-amyloid protein.

XX Synthetic.



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2004, 11:03:57 ; Search time 11 Seconds

(without alignments)  
85,206 Million cell updates/sec

Title: US-09-847-586-77  
Perfect score: 89  
Sequence: 1 AKSPVKEAKSPERAKSP 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	1026	1 NFM_HUMAN	P12036 homo sapien
2	76	85.4	831	1 NFM_RAT	P16884 ratius norv
3	76	85.4	1087	1 NFM_MOUSE	P19246 mus musculu
4	59.5	66.9	915	1 NFM_HUMAN	P07197 homo sapien
5	51.5	57.9	6632	1 UN89_CAEEL	O01761 caenorhabdi
6	51	57.3	1815	1 SHK3_RAT	Q09114 ratius norv
7	50	56.2	810	1 NFM_BOVIN	O77788 bos taurus
8	49	55.1	113	1 H2B_OILIT	P82887 clisiodisc
9	48.5	54.5	848	1 NFM_MOUSE	P08553 mus musculu
10	48.5	54.5	218	1 H14_HUMAN	P10412 homo sapien
11	48	53.9	206	1 H1_ONCMY	P06350 oncorhynch
12	48	53.9	216	1 H1_C1_XENLA	P15865 xenopus lae
13	48	53.9	217	1 H1_ANAPL	P09426 anas platyr
14	48	53.9	217	1 H1_CHICK	P09987 gallus galli
15	48	53.9	218	1 H101_CHICK	P08284 gallus galli
16	48	53.9	219	1 H101_CHICK	P08286 gallus galli
17	48	53.9	220	1 H102_CHICK	P15865 xenopus lae
18	48	53.9	222	1 H15_MOUSE	P43276 mus musculu
19	48	53.9	225	1 H15_HUMAN	P16401 homo sapien
20	48	53.9	845	1 NFM_RAT	P18430 ratius norv
21	48	53.9	857	1 NFM_CHICK	P16053 gallus galli
22	47.5	53.4	209	1 H1A_XENLA	P06893 xenopus lae
23	47.5	53.4	220	1 H13_MOUSE	P43277 mus musculu
24	47.5	53.4	248	1 H1_PARAN	P02256 paracichn
25	47	52.8	205	1 H1E_STRPU	P19376 strongyloc
26	47	52.8	218	1 H1E_CHICK	P08288 gallus galli
27	47	52.8	223	1 H103_CHICK	P08285 gallus galli
28	47	52.8	224	1 H111_CHICK	P08287 gallus galli
29	47	52.8	233	1 H11_GLYBA	P40263 glyptotendi
30	47	52.8	484	1 MEC2_MOUSE	Q92246 mus musculu
31	47	52.8	486	1 MEC2_HUMAN	P15608 homo sapien
32	47	52.8	492	1 MEC2_RAT	P00566 rattus norv
33	46.5	52.2	219	1 H1B_XENLA	P06893 xenopus lae

34	46.5	52.2	220	1 H13_HUMAN	P16402 homo sapien
35	46.5	52.2	238	1 H1_WHEAT	P27806 triticum ae
36	46	51.7	211	1 H12_MOUSE	P15864 mus musculu
37	46	51.7	1007	1 PR4B_MOUSE	Q61136 mus musculu
38	45.5	51.1	194	1 H5B_XENLA	P22845 xenopus lae
39	45.5	51.1	196	1 H5A_XENLA	P22844 xenopus lae
40	45	50.6	559	1 DAC3_HUMAN	Q9by19 homo sapien
41	45	50.6	1130	1 YL17_CAEEL	O11102 caenorhabdi
42	44.5	50.0	159	1 H2A_WATZE	P40280 zea mays (m
43	44.5	50.0	171	1 H1_ECHCR	P02257 echinolaempa
44	44.5	50.0	194	1 H1_SALTR	P02254 salmo trutt
45	44.5	50.0	213	1 H13_RABIT	P02251 oryctolagus

## ALIGNMENTS

RESULT 1  
ID NFM\_HUMAN STANDARD; PRT; 1026 AA.  
AC P12036; Q9UQ14;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Neurofilament triplet H protein (200 kDa neurofilament protein)  
DE (Neurofilament heavy polypeptide) (NF-H).  
GN NEFH OR NFM OR KIA0845.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=68328981; PubMed=3138108;  
RX MEDLINE=9156230; PubMed=10048485;  
RA Nagase T, Ishikawa K.-I., Suyama M, Kikuno R, Hiroseawa M, Miyajima N, Tanaka A, Kotani H, Nomura N, Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";  
RL DNA Res. 5:355-364 (1998).  
- FUNCTION: Neurofilaments usually contain three intermediate filament proteins: L, M, and H which are involved in the maintenance of neuronal caliber. NF-H has an important function in mature axons that is not subverted by the two smaller NF proteins.  
- PTM: There are a number of repeats of the tripeptide K-S-P, NFM is thought that phosphorylation of NFM results in the formation of interfilament cross bridges that are important in the maintenance of axonal caliber.  
- PTM: Phosphorylation seems to play a major role in the functioning of the larger neurofilament polypeptides (NF-M and NF-H), the levels of phosphorylation being altered developmentally and coincident with a change in the neurofilament filament function.  
- SIMILARITY: Belongs to the intermediate filament family.  
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CC EMBL; X15306; CA33366.1; JOINED.  
 CC EMBL; X15307; CA33366.1; JOINED.  
 CC EMBL; X15308; CA33366.1; JOINED.  
 CC EMBL; X15309; CA33366.1; JOINED.  
 CC EMBL; AF203032; AAF13722.1; JOINED.  
 CC EMBL; AB020652; BAA74868.2; JOINED.  
 CC PIR; S00979; QFHUH.  
 CC Genbank; HGNC:7737; NEFH.  
 CC MIM; 162230; NEFH.  
 CC GO; GO:0005983; C:neurofilament; NAS.  
 CC GO; GO:0007359; P:neurogenesis; NAS.  
 CC InterPro; IPR01664; IF.  
 CC Pfam; PF00038; filament; 1.  
 CC Prosite; PS00226; IF; 1.  
 CC DR Intermediate filament; Coiled coil; Neurone; Phosphorylation; Repeat.  
 CC KW Intermediate filament; Coiled coil; Neurone; Phosphorylation; Repeat.  
 CC FT DOMAIN 1 100 HEAD.  
 CC FT DOMAIN 101 413 ROD.  
 CC FT DOMAIN 102 1026 TAIL.  
 CC FT DOMAIN 101 132 COIL 1A.  
 CC FT DOMAIN 133 145 LINKER 1.  
 CC FT DOMAIN 146 244 COIL 1B.  
 CC FT DOMAIN 245 266 LINKER 12.  
 CC FT DOMAIN 267 292 COIL 2A.  
 CC FT DOMAIN 289 292 LINKER 2.  
 CC FT DOMAIN 293 413 COIL 2B.  
 CC FT CONFLICT 656 MISSING (IN REF. 1).  
 CC FT CONFLICT 811 E -> A (IN REF. 1).  
 CC SQ SEQUENCE 1026 AA; 112478 MW; 0879B6A08D208C17 CRC64;

Query March Best Local Similarity 100.0%; Score 89; DB 1; Length 1026;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSPYKEAKSPKAKSP 18  
 DB 700 AKSPYKEAKSPKAKSP 717

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RESULT 2  
 NFEH\_RAT  
 ID NFEH\_RAT STANDARD; PRT; 831 AA.  
 AC P16884; Q63368;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurofilament triplet H protein (200 kDa neurofilament protein)  
 DE (Neurofilament heavy polypeptide) (NF-H) (Fragment).  
 GN NFEH OR NFEH.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=89065087; PubMed=2143606;  
 RA Breen K.C., Robinson P.A., Wion D., Anderson B.H.;  
 RT "Partial sequence of the rat heavy neurofilament polypeptide (NF-H).  
 RT Identification of putative phosphorylation sites.";  
 RL FEBS Lett. 241:213-216(1988).  
 RP [2]  
 RP SEQUENCE OF 37-831 FROM N.A.  
 RX MEDLINE=88309090; PubMed=2457365;  
 RA Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L.,  
 RA Jolles P.;  
 RT "The large neurofilament subunit (NF-H) of the rat: cDNA cloning and  
 RT in situ detection.";  
 RL Biochem. Biophys. Res. Commun. 154:1099-1106(1988).  
 RP [3]  
 RP SEQUENCE OF 1-89 AND 243-313 FROM N.A.

RX MEDLINE=87080760; PubMed=2878828;  
 RA Robinson P.A., Wion D., Anderson B.H.;  
 RT "Isolation of a cDNA for the rat heavy neurofilament polypeptide  
 RT (NF-H).";  
 RL FEBS Lett. 209:203-205(1986).  
 RN [4]  
 RP SEQUENCE OF 318-831 FROM N.A.  
 RX MEDLINE=89184647; PubMed=2928342;  
 RA Lieberburg I., Spinner N., Snyder S., Anderson J., Goldhaber D.,  
 RA Smolowitz M., Carroll Z., Emanuel B.S., Brinher J., Rubin L.;  
 RT "Cloning of a cDNA encoding the rat high molecular weight  
 RT neurofilament peptide (NF-H): developmental and tissue expression in  
 RT the rat, and mapping of its human homologue to chromosomes 1 and  
 RT 22.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2463-2467(1989).  
 CC -1- FUNCTION: Neurofilaments usually contain three intermediate  
 CC filament proteins: L, M, and H which are involved in the  
 CC maintenance of neuronal caliber. NF-H has an important function in  
 CC mature axons that is not subverted by the two smaller NF proteins.  
 CC -1- PTM: There are a number of repeats of the tripeptide K-S-P, NFH is  
 CC phosphorylated on a number of the serines in this motif. It is  
 CC thought that phosphorylation of NFH results in the formation of  
 CC intermediate cross bridges that are important in the maintenance  
 CC of axonal caliber.  
 CC -1- PTM: Phosphorylation seems to play a major role in the functioning  
 CC of the larger neurofilament polypeptides (NF-H and NF-M), the  
 CC levels of phosphorylation being altered developmentally and  
 CC coincident with a change in the neurofilament function.  
 CC -1- SIMILARITY: Belongs to the intermediate filament family.  
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a  
 CC frameshift in position 783.

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 CC use by non-profit institutions as long as its content is in no way  
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CC EMBL; M37227; AAA41693.1; ALT\_FRAME.  
 CC EMBL; X13804; CA32038.1; ALT\_FRAME.  
 CC DR EMBL; M21964; AAA41695.1; -;  
 CC DR EMBL; J04517; AAA41692.1; -;  
 CC DR PIR; S02003; S02003.  
 CC DR InterPro; IPR001664; IF.  
 CC DR Pfam; PF00038; filament; 1.  
 CC DR Prosite; PS00226; IF; 1.  
 CC KW Intermediate filament; Coiled coil; Neurone; Phosphorylation; Repeat.  
 CC FT NON\_TER 1 1  
 CC FT DOMAIN 276 641  
 CC FT CONFLICT 164 164 L -> I (IN REF. 2).  
 CC FT CONFLICT 165 185 I -> S (IN REF. 2).  
 CC FT CONFLICT 193 193 L -> T (IN REF. 2).  
 CC FT CONFLICT 199 199 M -> T (IN REF. 2).  
 CC FT CONFLICT 199 199 K -> N (IN REF. 1).  
 CC FT CONFLICT 346 346 M -> N (IN REF. 1).  
 CC FT CONFLICT 373 373 A -> V (IN REF. 1 AND 4).  
 CC FT CONFLICT 482 482 G -> E (IN REF. 2 AND 4).  
 CC FT CONFLICT 485 485 P -> S (IN REF. 2).  
 CC FT CONFLICT 570 571 RK -> KE (IN REF. 2 AND 4).  
 CC FT CONFLICT 591 591 P -> T (IN REF. 2 AND 4).  
 CC FT CONFLICT 727 727 A -> V (IN REF. 4).  
 CC FT CONFLICT 757 759 AAP -> GST (IN REF. 4).  
 CC FT CONFLICT 769 769 R -> L (IN REF. 2).  
 CC FT CONFLICT 775 775 R -> P (IN REF. 2 AND 4).  
 CC SQ SEQUENCE 831 AA; 89486 MW; 180973C3F135F768 CRC64;

Query March Best Local Similarity 85.4%; Score 76; DB 1; Length 831;  
 Matches 18; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 AKSPYKEAKSPKAKSP 18  
 DB 700 AKSPYKEAKSPKAKSP 717